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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/000,321

DATE: 01/26/2002

TIME: 13:42:58

Input Set : N:\Crf3\RULE60\10000321.raw

Output Set: N:\CRF3\01252002\J000321.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: BRUST, Stefan
 6 KNAPP, Stefan
 7 GERKEN, Manfred
 8 GUERTLER, Lutz

10 (ii) TITLE OF INVENTION: Peptides derived from a retrovirus of
 11 the HIV group, and their use

13 (iii) NUMBER OF SEQUENCES: 11

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Foley & Lardner
 17 (B) STREET: 3000 K Street, N.W., Suite 500
 18 (C) CITY: Washington
 19 (D) STATE: D.C.
 20 (E) COUNTRY: USA
 21 (F) ZIP: 20007-5109

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

ENTERED

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/000,321
 C--> 31 (B) FILING DATE: 04-Dec-2001
 32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/131,551
 36 (B) FILING DATE:

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: SANDERCOCK, Colin G.
 40 (B) REGISTRATION NUMBER: 31,298
 41 (C) REFERENCE/DOCKET NUMBER: 58315/106/BEAK

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (202)672-5300
 45 (B) TELEFAX: (202)672-5399
 46 (C) TELEX: 904136

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:
 52 (A) LENGTH: 48 amino acids
 53 (B) TYPE: amino acid
 54 (C) STRANDEDNESS:
 55 (D) TOPOLOGY: linear

59 (ix) FEATURE:

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60 (A) NAME/KEY: Modified-site
61 (B) LOCATION: 29
62 (D) OTHER INFORMATION: /note= "Xaa represents Cys or Ser"
64 (ix) FEATURE:
65 (A) NAME/KEY: Modified-site
66 (B) LOCATION: 35
67 (D) OTHER INFORMATION: /note= "Xaa represents Cys or Ser"
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 Val Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr
73 1 5 10 15
W--> 75 Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu Trp Gly Xaa Lys Gly Lys
76 20 25 30
W--> 78 Leu Ile Xaa Tyr Thr Ser Val Lys Trp Asn Thr Ser Trp Ser Gly Arg
79 35 40 45
82 (2) INFORMATION FOR SEQ ID NO: 2:
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 23 amino acids
86 (B) TYPE: amino acid
87 (C) STRANDEDNESS:
88 (D) TOPOLOGY: linear
94 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96 Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys
97 1 5 10 15
99 Tyr Thr Ser Val Lys Trp Asn
100 20
102 (2) INFORMATION FOR SEQ ID NO: 3:
104 (i) SEQUENCE CHARACTERISTICS:
105 (A) LENGTH: 26 amino acids
106 (B) TYPE: amino acid
107 (C) STRANDEDNESS:
108 (D) TOPOLOGY: linear
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
116 Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
117 1 5 10 15
119 Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys
120 20 25
122 (2) INFORMATION FOR SEQ ID NO: 4:
124 (i) SEQUENCE CHARACTERISTICS:
125 (A) LENGTH: 26 amino acids
126 (B) TYPE: amino acid
127 (C) STRANDEDNESS:
128 (D) TOPOLOGY: linear
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
136 Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
137 1 5 10 15
139 Leu Trp Gly Ser Lys Gly Lys Leu Ile Ser
140 20 25
142 (2) INFORMATION FOR SEQ ID NO: 5:
144 (i) SEQUENCE CHARACTERISTICS:

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Input Set : N:\Crf3\RULE60\10000321.raw
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145 (A) LENGTH: 23 amino acids
 146 (B) TYPE: amino acid
 147 (C) STRANDEDNESS:
 148 (D) TOPOLOGY: linear
 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 156 Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys
 157 1 5 10 15
 159 Thr Thr Ala Val Pro Trp Asn
 160 20
 162 (2) INFORMATION FOR SEQ ID NO: 6:
 164 (i) SEQUENCE CHARACTERISTICS:
 165 (A) LENGTH: 26 amino acids
 166 (B) TYPE: amino acid
 167 (C) STRANDEDNESS:
 168 (D) TOPOLOGY: linear
 174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 176 Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
 177 1 5 10 15
 179 Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys
 180 20 25
 182 (2) INFORMATION FOR SEQ ID NO: 7:
 184 (i) SEQUENCE CHARACTERISTICS:
 185 (A) LENGTH: 26 amino acids
 186 (B) TYPE: amino acid
 187 (C) STRANDEDNESS:
 188 (D) TOPOLOGY: linear
 194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 196 Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
 197 1 5 10 15
 199 Ile Trp Gly Ser Ser Gly Lys Leu Ile Ser
 200 20 25
 202 (2) INFORMATION FOR SEQ ID NO: 8:
 204 (i) SEQUENCE CHARACTERISTICS:
 205 (A) LENGTH: 32 base pairs
 206 (B) TYPE: nucleic acid
 207 (C) STRANDEDNESS: single
 208 (D) TOPOLOGY: linear
 214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 216 TGTGTGGTAC CGCAGCGGCA ACAGCGCTGA CG 32
 218 (2) INFORMATION FOR SEQ ID NO: 9:
 220 (i) SEQUENCE CHARACTERISTICS:
 221 (A) LENGTH: 32 base pairs
 222 (B) TYPE: nucleic acid
 223 (C) STRANDEDNESS: single
 224 (D) TOPOLOGY: linear
 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 232 GTGTGTCTAG TTTAGTTATG TCAAACCAAT TC 32
 234 (2) INFORMATION FOR SEQ ID NO: 10:
 236 (i) SEQUENCE CHARACTERISTICS:

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Input Set : N:\Crf3\RULE60\10000321.raw
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237 (A) LENGTH: 146 amino acids
 238 (B) TYPE: amino acid
 239 (C) STRANDEDNESS:
 240 (D) TOPOLOGY: linear
 246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 248 Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser Val Leu Lys Gly Ile
 249 1 5 10 15
 251 Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln Gln His
 252 20 25 30
 254 Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu
 255 35 40 45
 257 Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu Trp
 258 50 55 60
 260 Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Thr
 261 65 70 75 80
 263 Ser Trp Ser Gly Arg Tyr Asn Asp Asp Ser Ile Trp Asp Asn Leu Thr
 264 85 90 95
 266 Trp Gln Gln Trp Asp Gln His Ile Asn Asn Val Ser Ser Ile Ile Tyr
 267 100 105 110
 269 Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln Glu Lys Asn Val Lys Ala
 270 115 120 125
 272 Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile
 273 130 135 140
 275 Thr Lys
 276 145
 278 (2) INFORMATION FOR SEQ ID NO: 11:
 280 (i) SEQUENCE CHARACTERISTICS:
 281 (A) LENGTH: 145 amino acids
 282 (B) TYPE: amino acid
 283 (C) STRANDEDNESS:
 284 (D) TOPOLOGY: linear
 290 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 292 Val Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile
 293 1 5 10 15
 295 Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His
 296 20 25 30
 298 Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Val
 299 35 40 45
 301 Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile Trp
 302 50 55 60
 304 Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala
 305 65 70 75 80
 307 Ser Trp Ser Asn Lys Ser Leu Glu Asp Ile Trp Asp Asn Met Thr Trp
 308 85 90 95
 310 Met Gln Trp Glu Arg Glu Ile Asp Asn Tyr Thr Asn Thr Ile Tyr Thr
 311 100 105 110
 313 Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu
 314 115 120 125
 316 Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Ser Ile Thr

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Input Set : N:\Crf3\RULE60\10000321.raw
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317 130 135 140
319 Asn
320 145

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/000,321

DATE: 01/26/2002

TIME: 13:42:59

Input Set : N:\Crf3\RULE60\10000321.raw
Output Set: N:\CRF3\01252002\J000321.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1